

**Table S1.** Summary of RNA-Seq reads data

Group	Reads (bp)	Average Reads (bp)
	41940544	
HCT-116-Con	42894894	
	40503994	
	39947436	
HCT-116-Fuc	39650116	40044456.17 ± 1791724.56
	41084662	
	36904668	
HT-29-Con	37911654	
	39665026	
	41471420	
HT-29-Fuc	40758930	
	37800130	

**Table S2.** The top 15 up- and down-regulated genes in control and L-fucose treatment group for HCT-116 cells by RNA-seq analysis.

Gene	Description	Fold change (log <sub>2</sub> )	p-value	FDR
<b>UP-REGULATED GENES</b>				
<i>RNU4-23P</i>	RNA, U4 small nuclear 23, pseudogene	5.40	0.0027	0.515
<i>MIR6753</i>	microRNA 6753	4.83	0.0072	0.665
<i>AL023875.1</i>	TEC	4.69	0.0143	0.783
<i>DGCR10</i>	DiGeorge syndrome critical region gene 10	4.52	0.0217	0.815
<i>LINC01659</i>	long intergenic non-protein coding RNA 1659	4.52	0.0189	0.805
<i>AC091305.1</i>	TEC	4.51	0.0215	0.810
<i>AC073439.1</i>	TEC	4.34	0.0339	0.879
<i>AL355864.2</i>	ribosomal protein S2 (RPS2) pseudogene	4.33	0.0334	0.879
<i>AC087650.1</i>	ribosomal protein L29(RPL29) pseudogene	4.32	0.0452	0.916
<i>HTRA3</i>	HtrA serine peptidase 3	4.26	1.14E-11	5.58E-08
<i>SMC5-AS1</i>	SMC5 antisense RNA 1 (head to head)	3.45	0.0105	0.724
<i>RARRES2P4</i>	retinoic acid receptor responder 2 pseudogene 4	3.45	0.0277	0.861
<i>CDC27P1</i>	cell division cycle 27 pseudogene 1	3.37	0.0158	0.793
<i>HHATL-AS1</i>	HHATL antisense RNA 1	3.35	0.0149	0.783
<i>RPL23AP84</i>	ribosomal protein L23a pseudogene 84	3.34	0.0007	0.304
<b>DOWN-REGULATED GENES</b>				
<i>KRT18P5</i>	keratin 18 pseudogene 5	-5.13	0.0025	0.492
<i>AP000346.4</i>	rhabdoid tumor deletion region gene 1 (RTDR1) pseudogene	-5.12	0.0037	0.572
<i>AC004039.1</i>	novel transcript, antisense to KIF3A	-4.99	0.0051	0.633
<i>AC005274.1</i>	TEC	-4.74	0.0096	0.716
<i>LINC01635</i>	long intergenic non-protein coding RNA 1635	-4.61	0.0148	0.783
<i>AP001767.4</i>	TEC	-4.61	0.0148	0.783
<i>AL157827.2</i>	Novel transcript, antisense to CENPP	-4.61	0.0100	0.716
<i>SNORA2C</i>	small nucleolar RNA, H/ACA box 2C	-4.61	0.0156	0.788
<i>GULOP</i>	gulonolactone (L-) oxidase, pseudogene	-4.59	0.0264	0.856
<i>LMF1-AS1</i>	LMF1 antisense RNA 1	-4.47	0.0364	0.882
<i>YWHAQP7</i>	YWHAQ pseudogene 7	-4.44	0.0196	0.805
<i>THOC7-AS1</i>	THOC7 antisense RNA 1	-4.28	0.0488	0.921
<i>Z98885.1</i>	suppressor of cytokine signaling 2 (SOCS2) pseudogene	-4.25	0.0366	0.882
<i>STXBP5-AS1</i>	STXBP5 antisense RNA 1	-3.75	0.0006	0.276

<i>DCUN1D2-AS</i>	DCUN1D2 antisense RNA	-3.43	0.0201	0.805
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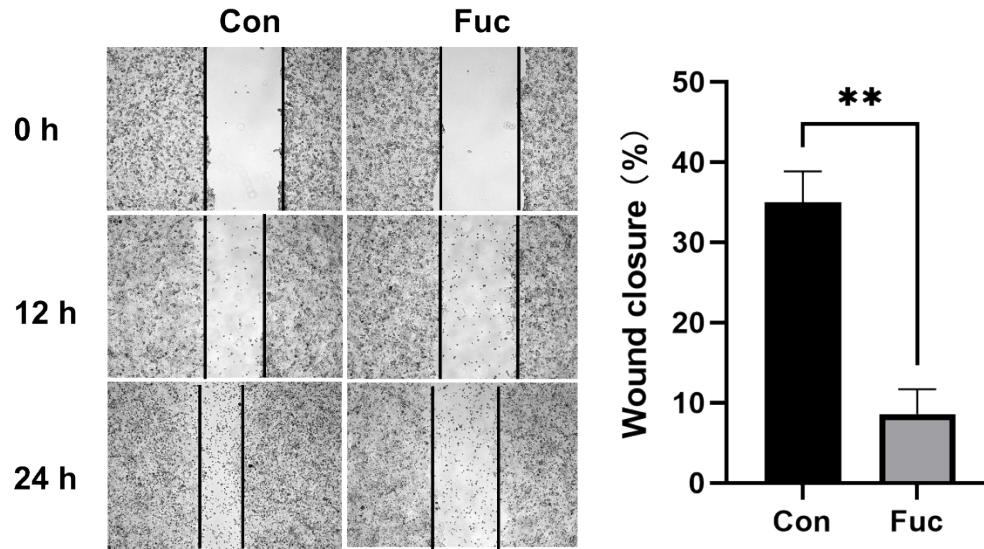
**Table S3.** The top 15 up- and down-regulated genes in control and L-fucose treatment group for HCT-29 cells by RNA-seq analysis.

Gene	Description	Fold change (log <sub>2</sub> )	p-value	FDR
<b>UP-REGULATED GENES</b>				
<i>AKR1C7P</i>	aldo-keto reductase family 1 member C7, pseudogene	5.69	0.0003	0.195
<i>AL157813.1</i>	novel transcript, sense intronic to RCBTB2	5.08	0.0024	0.403
<i>AC130371.1</i>	novel transcript, antisense to B3GNTL1	4.88	0.0080	0.615
<i>GGTA2P</i>	glycoprotein, alpha-galactosyltransferase 2, pseudogene	4.88	0.0080	0.615
<i>AP005212.2</i>	sorting nexin 18 (SNX18) pseudogene	4.87	0.0050	0.554
<i>MYO5BP1</i>	myosin VB pseudogene 1	4.85	0.0062	0.586
<i>AC007613.1</i>	novel transcript, antisense to TXNDC11	4.85	0.0037	0.475
<i>AC007620.3</i>	novel transcript, antisense to GNB4	4.60	0.0181	0.756
<i>AC068338.3</i>	novel transcript, antisense to NEIL1	4.58	0.0139	0.709
<i>AC136443.1</i>	phospholipase A2, group X (PLA2G10) pseudogene	4.44	0.0247	0.826
<i>DGCR10</i>	DiGeorge syndrome critical region gene 10	4.43	0.0208	0.781
<i>FAM242F</i>	family with sequence similarity 242 member F	4.43	0.0206	0.779
<i>DUSP5P1</i>	dual specificity phosphatase 5 pseudogene 1	4.42	0.0235	0.814
<i>AP006289.1</i>	ATP synthase subunit g, mitochondrial (ATP5L)pseudogene	4.41	0.0195	0.770
<i>DUTP6</i>	deoxyuridine triphosphatase pseudogene 6	4.26	0.0454	0.912
<b>DOWN-REGULATED GENES</b>				
<i>KRT18P55</i>	keratin 18 pseudogene 55	-5.76	6.72E-05	0.119
<i>VNIR108P</i>	vomer nasal 1 receptor 108 pseudogene	-4.55	0.0197	0.771
<i>DHRX-IT1</i>	DHRX intronic transcript 1	-4.55	0.0170	0.743
<i>AC007956.1</i>	ribosomal protein S2 (RPS2) pseudogene	-4.37	0.0424	0.907
<i>AL022238.3</i>	novel transcript, antisense to MKL1	-4.36	0.0305	0.842
<i>AL139124.1</i>	novel transcript, antisense to PLCE1	-4.36	0.0305	0.842
<i>MRPL35P2</i>	mitochondrial ribosomal protein L35 pseudogene 2	-4.15	0.0470	0.924
<i>AL035071.2</i>	novel transcript, antisense to MAPRE1	-4.01	0.0003	0.185
<i>AC022079.2</i>	novel transcript, antisense to CCDC91	-3.59	0.0031	0.430
<i>AL161909.1</i>	ribosomal protein S6 (RPS6) pseudogene	-3.40	0.0088	0.619
<i>LINC01473</i>	long intergenic non-protein coding RNA 1473	-3.39	0.0179	0.752
<i>ALGIL8P</i>	asparagine-linked glycosylation 1-like 8,	-3.30	0.0146	0.710

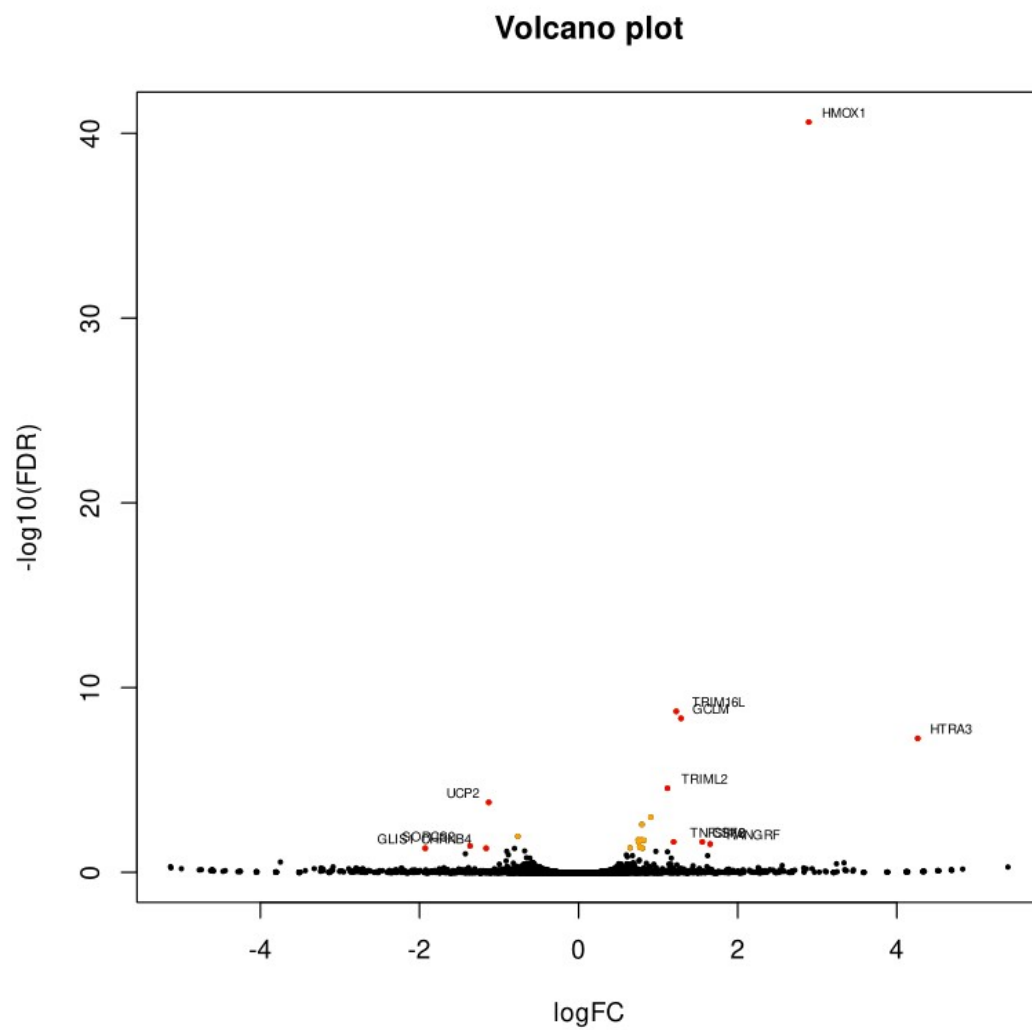
pseudogene				
<i>MTND4P9</i>	MT-ND4 pseudogene 9	-3.29	0.0080	0.615
<i>AL732314.6</i>	novel transcript, antisense to PPP2R3B	-3.27	0.0374	0.880
<i>HNRNPA1P3</i>	heterogeneous nuclear ribonucleoprotein A1	-3.04	0.0296	0.838
3	pseudogene 33			

**Table S4.** Sequences of primers used in research

Gene	Sequences
<i>FUT2</i>	F: 5' -CTACCACCTGAACGACTGGATG-3' R: 5' -AGGGTGAACCTCCTGGAGGATCT-3'
<i>FUT8</i>	F: 5' -GACAGAACTGGTTCAGCGGAGA-3' R: 5' -GCAGTAGACCACATGATGGAGC-3'
<i>FUK</i>	F: 5' -GCTCAATGACCACCTGCTCTTG-3' R: 5' -TCAGTTTGCCGTACCAGGCTGT-3'
<i>FPGT</i>	F: 5' - CAGATTGGGGCCTGATGTTTC -3' R: 5' - TCAAGTTGTCTTGCACTCCAAA -3'
<i>PSPH</i>	F: 5' -GACAGCACGGTCATCAGAGAAG-3' R: 5' -CGCTCTGTGAGAGCAGCTTTGA-3'
<i>GCAT</i>	F: 5' -TCTATGGCTGCCAAGACCCAGA-3' R: 5' -CTCTCTTCAGCATGTCATCCGC-3'
<i>SERPINE1</i>	F: 5' -CTCATCAGCCACTGGAAAGGCA-3' R: 5' -GACTCGTGAAGTCAGCCTGAAAC-3'
<i>PSAT1</i>	F: 5' -ACTTCCTGTCCAAGCCAGTGGA-3' R: 5' -CTGCACCTTGTATTCCAGGACC-3'
<i>GAPDH</i>	F: 5' -GTCAAGGCTGAGAACGGGAA- 3' R: 5' -AAATGAGCCCCAGCCTTCTC - 3'

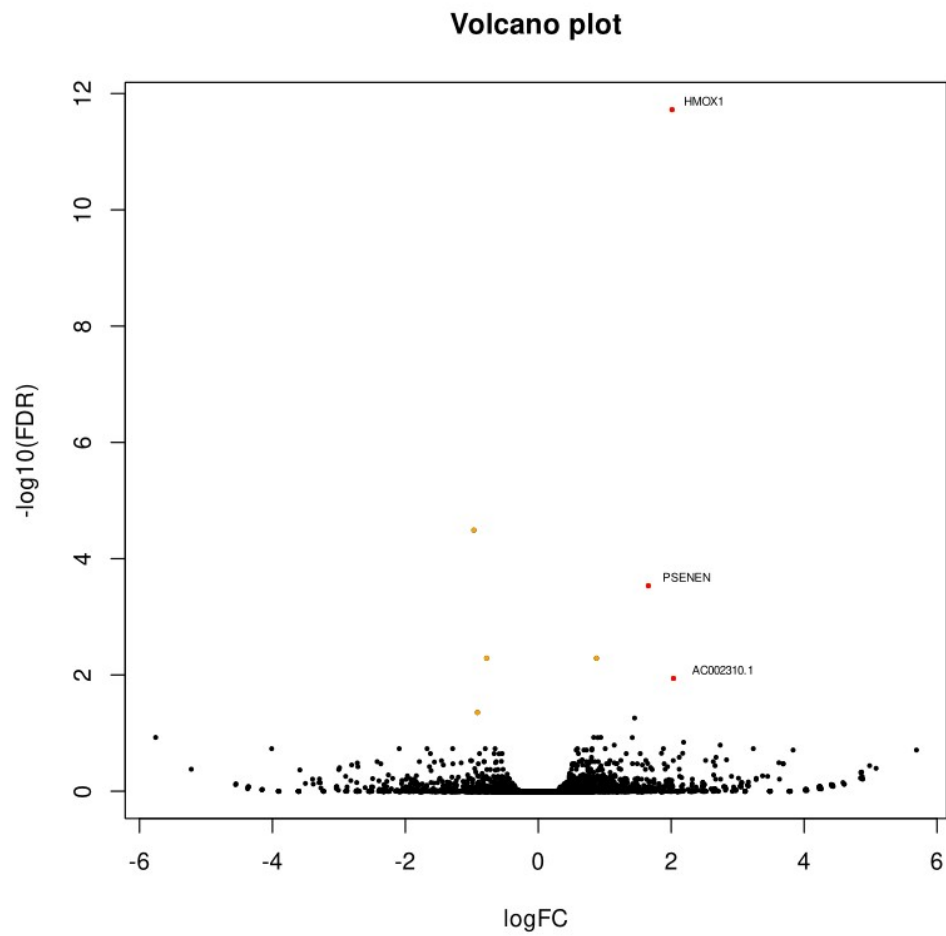


**Figure S1** Cell migration of HCT-116 cells with supplemental L-fucose determined by the wound healing assays.

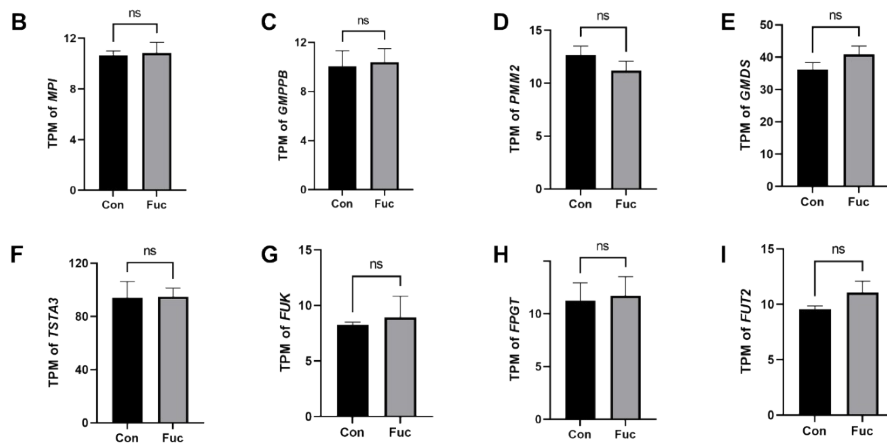
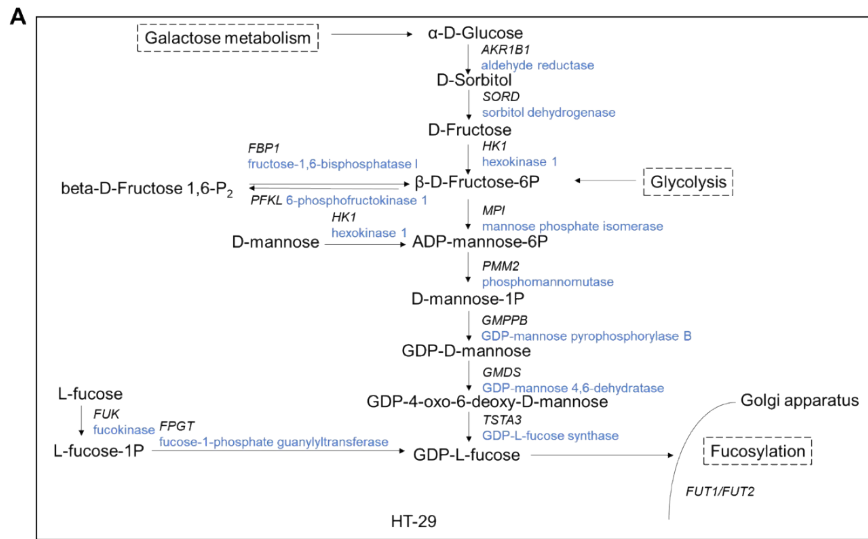


**Figure S2** Volcano plot shows ( $\log_2$ ) fold change in gene expression of HCT-116 cells treated with L-fucose compared with untreated control, plotted against significance ( $-\log_{10}[\text{FDR value}]$ ).

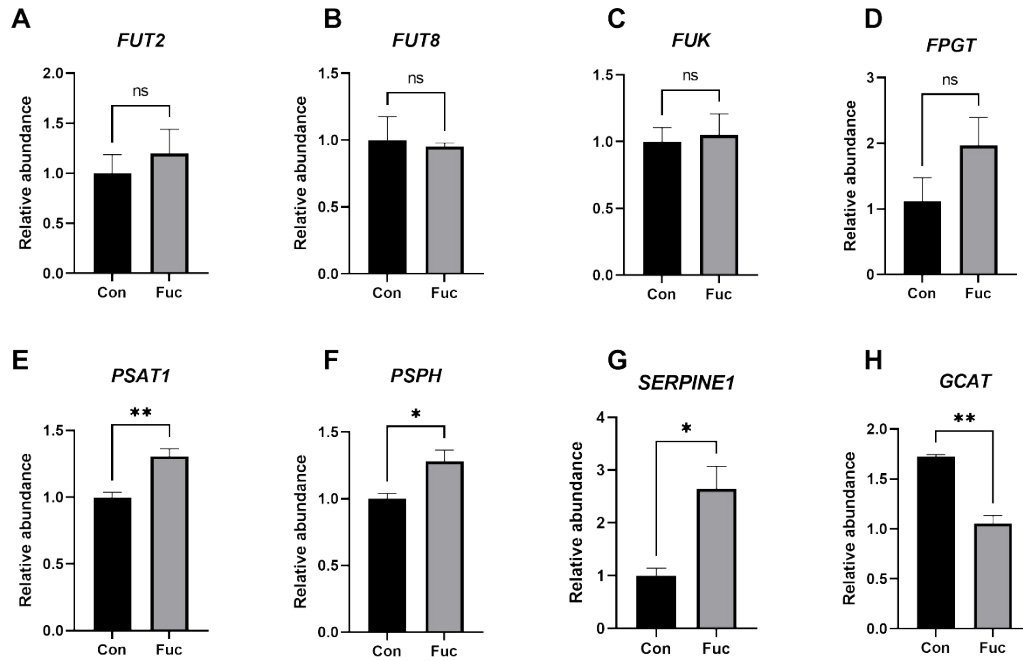
Significant genes ( $P < 0.05$ ) are represented in red.



**Figure S3** Volcano plot shows ( $\log_2$ ) fold change in gene expression of HT-29 cells treated with L-fucose compared with untreated control, plotted against significance ( $-\log_{10}[\text{FDR value}]$ ). Significant genes ( $P < 0.05$ ) are represented in red.



**Figure S4 A**, Genes involved in the exogenous fucose metabolic pathway of HT-29 cells. **B**, fold change of mRNA expression for the genes encoding key enzymes in exogenous and endogenous fucose metabolic pathways in HT-29 cells. n = 3 samples/group.



**Figure S5** Quantitative real-time PCR assays of genes in HCT-116 cells identified by RNA-seq. The mRNA levels of genes were normalized to GAPDH. Relative mRNA levels of genes in L-fucose group were compared to the control group, where the expression was set to 1.0 ( $n = 3$ ; values represent mean  $\pm$  SEM). An unpaired Student's t-test was used to assess statistically significant differences (compared to control \* $P < 0.05$ ; \*\* $P < 0.01$ ; ns, no significance).